Claims:

1. An isolated polynucleotide comprising a polynucleotide sequence which codes for the metY gene of corneyform bacteria, selected from the group consisting of

   a) polynucleotide which is at least 70% identical to a polynucleotide that codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

   b) polynucleotide which codes for a polypeptide that comprises an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID No. 2,

   c) polynucleotide which is complementary to the polynucleotides of a) or b), and

   d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

2. The polynucleotide of claim 1, which is capable of replication in coryneform bacteria.

3. The polynucleotide of claim 1, wherein the polynucleotide is an RNA.

4. The polynucleotide of claim 2, comprising the nucleic acid sequence of SEQ ID No. 1.

5. The DNA of claim 2 which is capable of replication, comprising

   (i) the nucleotide sequence shown in SEQ ID No. 1, or

   (ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with a sequence complementary to sequence (i) or (ii), and optionally

(iv) sense mutations of (i).

6. The DNA of claim 5 which is capable of replication, wherein the hybridization of sequence (iii) occurs at a stringency corresponding to at most 2x SSC.

7. A polynucleotide sequence of claim 2, which codes for a polypeptide which comprises the amino acid sequence in SEQ ID No. 2.

8. Corynebacterium glutamicum strain DSM5715/pCREmetY as DSM 13556 deposited at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (German Collection of Microorganisms and Cell Cultures), Braunschweig, Germany.

9. A process for the fermentative preparation of L-amino acids, comprising:

a) fermentation of the coryneform bacteria which produce the desired amino acid and in which at least the metY gene or nucleotide sequences which code for it are enhanced;

b) concentration of the L-amino acid in the medium or in the cells of the bacteria; and

c) isolation of the L-amino acid.

10. A process for the fermentative preparation of L-methionine, comprising:

a) fermentation of an L-methionine-producing coryneform bacteria in which the metY gene, optionally with met A, is enhanced;

b) concentration of said L-amino acid in the medium or in the cells of the bacteria; and

c) isolation of said L-amino acid.

11. The process of claim 9 or 10, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

12. The process of claim 9 or 10, wherein bacteria in which the metabolic pathways which reduce the formation of the desired amino acid are at least partly eliminated are employed.

13. The process of claim 9, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the metY gene and optionally additionally the metA gene.

14. The process of claim 10, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the metA and metY genes.

15. The process of claim 9, wherein for the preparation of L-lysine, the coryneform microorganisms have one or more enhanced genes selected from the group consisting of

15.1 gap gene which codes for glycerolaldehyde 3-phosphate dehydrogenase,

15.2 tpi gene which codes for triose phosphate isomerase,

15.3 pgk gene which codes for 3-phosphoglycerate kinase,

15.4 pyc gene which codes for pyruvate carboxylase,

15.5 lysC gene which codes for a feed back resistant aspartate kinase.

16. The process of claim 10, wherein the coryneform microorganisms have one or more enhanced genes selected from the group consisting of

16.1 the lysC gene which codes for a feed back resistant aspartate kinase,

16.2 the gap gene which codes for glyceroldehyde 3-phosphate dehydrogenase,

16.3 the tpi gene which codes for triose phosphate isomerase,

16.4 the metA gene which codes for homoserine O-acetyltransferase,

16.5 the metB gene which codes for cystathionine-gamma-synthase,

16.6 the aecD gene which codes for cystathionine-gamma-lyase,

16.7 the glyA gene which codes for serine hydroxymethyltransferase

16.8 the pgk gene which codes for 3-phosphoglycerate kinase

16.9 the pyc gene which codes for pyruvate carboxylase.

17. The process of claim 16, wherein the coryneform microorganisms have an additional enhancement of the metY gene by metA.

18. The process of claim 9, wherein the coryneform microorganisms have an additional enhancement of the metY gene by attenuation of one or more genes selected from the group consisting of

18.1 the pck gene which codes for phosphoenol pyruvate carboxykinase

18.2 the pgi gene which codes for glucose 6-phosphate isomerase

18.3 the poxB gene which codes for pyruvate oxidase.

19. The process of claim 10, wherein the coryneform microorganisms have one or more attenuated genes selected from the group consisting of

19.1 the thrB gene which codes for homoserine kinase

19.2 the ilvA gene which codes for threonine dehydratase

19.3 the thrC gene which codes for threonine synthase

19.4 the ddh gene which codes for meso-diaminopimelate D-dehydrogenase

19.5 the pck gene which codes for phosphoenol pyruvate carboxykinase

19.6 the pgi gene which codes for glucose 6-phosphate isomerase

19.7 the poxB gene which codes for pyruvate oxidase.

20. A coryneform bacterium in which the metY gene is enhanced.

21. A coryneform bacterium that contains a vector which carries a polynucleotide of claim 1.

22. The process of claims 9 or 10, wherein microorganisms of the species Corynebacterium glutamicum are employed.

23. The process of claim 22, wherein the Corynebacterium glutamicum strain DSM5715/pCREmetY is employed.

24. The process of claim 22, wherein the Corynebacterium glutamicum strain DSM5715/pCREmetAY is employed.

25. A process for preparing an L-methionine-containing animal feedstuffs additive comprising:

a) culture and fermentation of an L-methionine-producing microorganism in a fermentation medium;

b) removal of water from the L-methionine-containing fermentation broth (concentration);

c) removal of an amount of 0 to 100 wt.% of the biomass formed during the fermentation; and

d) drying of the fermentation broth obtained according to b) and/or c) to obtain the animal feedstuffs additive in the desired powder or granule form.

26. The process of claim 25, wherein microorganisms are employed in which further genes of the biosynthesis pathway of L-methionine are additionally enhanced.

27. The process of claim 26, wherein microorganisms are employed in which the metabolic pathways which reduce the formation of L-methionine are at least partly eliminated.

28. The process of claim 25, wherein expression of the polynucleotides which code for the metY gene is enhanced.

29. The process of claim 25, wherein microorganisms of the species Corynebacterium glutamicum are employed.

30. The process of claim 29, wherein the Corynebacterium glutamicum strain DSM5715/pCREmetY is employed.

31. The process of claim 29, wherein the Corynebacterium glutamicum strain DSM5715/pCREmetAY is employed.

32. The process of claim 25, wherein one or more of the following steps are additionally carried out:

e) addition of one or more organic substances, including L-methionine and/or D-methionine and/or the racemic mixture D,L-methionine, to the products obtained according to b), c) and/or d);

f) addition of auxiliary substances selected from the group consisting of silicas, silicates, stearates, grits and bran to the substances obtained according

to b) to e) for stabilization and to increase storability; or

g) conversion of the substances obtained according to b) to f) into a form which remains stable in rumen, by coating them with film-forming agents.

33. The process of claim 25 or 32, wherein some of the biomass is removed.

34. The process of claim 33, wherein essentially 100% of the biomass is removed.

35. The process of claim 25 or 32, wherein the water content is up to 5 wt.%.

36. The process of claim 35, wherein the water content is less than 2 wt.%.

37. The process of claim 32, wherein the film-forming agents are metal carbonates, silicas, silicates, alginates, stearates, starches, gums or cellulose ethers.

38. An animal feedstuffs additive prepared as claimed in claim 25.

39. An animal feedstuffs additive as claimed in claim 38, which comprises 1 wt.% to 80 wt.% L-methionine, D-methionine, D,L-methionine or a mixture thereof, based on the dry weight of the animal feedstuffs additive.

40. A process for obtaining RNA, cDNA or DNA in order to isolate nucleic acids, or polynucleotides or genes which code for O-acetylhomoserine sulfhydrolase or which have a high similarity to the sequence of the metY gene, which comprises employing polynucleotides of claim 1 as hybridization probes.